

## SEQUENCE LISTING

&lt;110&gt; OriGene Technologies, Inc

&lt;120&gt; Human EphA6 Gene and Polypeptide

&lt;130&gt; OGT 16U 102 R1

&lt;160&gt; 9

&lt;170&gt; PatentIn version 3.0

&lt;210&gt; 1

&lt;211&gt; 3914

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (86)..(3196)

```

<400> 1
gaaggacccc catcctaccc agaacacctg cctgcgctgc cgccacttct ctttaaggga      60
gaggaaaaga gagcctagga gaacc atg ggg ggc tgc gaa gtc cgg gaa ttt      112
                               Met Gly Gly Cys Glu Val Arg Glu Phe
                               1                               5
ctt ttg caa ttt ggt ttc ttc ttg cct ctg ctg aca gcg tgg cca ggc      160
Leu Leu Gln Phe Gly Phe Phe Leu Pro Leu Leu Thr Ala Trp Pro Gly
10                               15                               20                               25
gac tgc agt cac gtc tcc aac aac caa gtt gtg ttg ctt gat aca aca      208
Asp Cys Ser His Val Ser Asn Asn Gln Val Val Leu Leu Asp Thr Thr
                               30                               35                               40
act gta ctg gga gag cta gga tgg aaa aca tat cca tta aat ggg tgg      256
Thr Val Leu Gly Glu Leu Gly Trp Lys Thr Tyr Pro Leu Asn Gly Trp
                               45                               50                               55
gat gcc atc act gaa atg gat gaa cat aat agg ccc att cac aca tac      304
Asp Ala Ile Thr Glu Met Asp Glu His Asn Arg Pro Ile His Thr Tyr
60                               65                               70
cag gta tgt aat gta atg gaa cca aac caa aac aac tgg ctt cgt aca      352
Gln Val Cys Asn Val Met Glu Pro Asn Gln Asn Asn Trp Leu Arg Thr
75                               80                               85
aac tgg atc tcc cgt gat gca gct cag aaa att tat gtg gaa atg aaa      400
Asn Trp Ile Ser Arg Asp Ala Ala Gln Lys Ile Tyr Val Glu Met Lys
90                               95                               100                               105
ttc aca cta agg gat tgt aac agc atc cca tgg gtc ttg ggg act tgc      448
Phe Thr Leu Arg Asp Cys Asn Ser Ile Pro Trp Val Leu Gly Thr Cys
110                               115                               120
aaa gaa aca ttt aat ctg ttt tat atg gaa tca gat gag tcc cac gga      496
Lys Glu Thr Phe Asn Leu Phe Tyr Met Glu Ser Asp Glu Ser His Gly
125                               130                               135
att aaa ttc aag cca aac cag tat aca aag atc gac aca att gct gct      544
Ile Lys Phe Lys Pro Asn Gln Tyr Thr Lys Ile Asp Thr Ile Ala Ala
140                               145                               150
gat gag agt ttt acc cag atg gat ttg ggt gat cgc atc ctc aaa ctc      592
Asp Glu Ser Phe Thr Gln Met Asp Leu Gly Asp Arg Ile Leu Lys Leu
155                               160                               165
aac act gaa att cgt gag gtg ggg cct ata gaa agg aaa gga ttt tat      640
Asn Thr Glu Ile Arg Glu Val Gly Pro Ile Glu Arg Lys Gly Phe Tyr
170                               175                               180                               185
ctg gct ttt caa gac att ggg gcg tgc att gcc ctg gtt tca gtc cgt      688
Leu Ala Phe Gln Asp Ile Gly Ala Cys Ile Ala Leu Val Ser Val Arg

```

16U 102 R1.ST25

190	195	200	
gtt ttc tac aag aaa tgc ccc ttc act gtt cgt aac ttg gcc atg ttt Val Phe Tyr Lys Lys Cys Pro Phe Thr Val Arg Asn Leu Ala Met Phe 205 210 215			736
cct gat acc att cca agg gtt gat tcc tcc tct ttg gtt gaa gta cgg Pro Asp Thr Ile Pro Arg Val Asp Ser Ser Ser Leu Val Glu Val Arg 220 225 230			784
ggt tct tgt gtg aag agt gct gaa gag cgt gac act cct aaa ctg tat Gly Ser Cys Val Lys Ser Ala Glu Glu Arg Asp Thr Pro Lys Leu Tyr 235 240 245			832
tgt gga gct gat gga gat tgg ctg gtt cct ctt gga agg tgc atc tgc Cys Gly Ala Asp Gly Asp Trp Leu Val Pro Leu Gly Arg Cys Ile Cys 250 255 260 265			880
agt aca gga tat gaa gaa att gag ggt tct tgc cat gct tgc aga cca Ser Thr Gly Tyr Glu Glu Ile Glu Gly Ser Cys His Ala Cys Arg Pro 270 275 280			928
gga ttc tat aaa gct ttt gct ggg aac aca aaa tgt tct aaa tgt cct Gly Phe Tyr Lys Ala Phe Ala Gly Asn Thr Lys Cys Ser Lys Cys Pro 285 290 295			976
cca cac agt tta aca tac atg gaa gca act tct gtc tgt cag tgt gaa Pro His Ser Leu Thr Tyr Met Glu Ala Thr Ser Val Cys Gln Cys Glu 300 305 310			1024
aag ggt tat ttc cga gct gaa aaa gac cca cct tct atg gca tgt acc Lys Gly Tyr Phe Arg Ala Glu Lys Asp Pro Pro Ser Met Ala Cys Thr 315 320 325			1072
agg cca cct tca gct cct agg aat gtg gtt ttt aac atc aat gaa aca Arg Pro Pro Ser Ala Pro Arg Asn Val Val Phe Asn Ile Asn Glu Thr 330 335 340 345			1120
gcc ctt att ttg gaa tgg agc cca cca agt gac aca gga ggg aga aaa Ala Leu Ile Leu Trp Ser Pro Pro Ser Asp Thr Gly Gly Arg Lys 350 355 360			1168
gat ctc aca tac agt gta atc tgt aag aaa tgt ggc tta gac acc agc Asp Leu Thr Tyr Ser Val Ile Cys Lys Lys Cys Gly Leu Asp Thr Ser 365 370 375			1216
gag tgt gag gac tgt ggt gga gga ctc cgc ttc atc cca aga cat aca Gln Cys Glu Asp Cys Gly Gly Gly Leu Arg Phe Ile Pro Arg His Thr 380 385 390			1264
ggc ctg atc aac aat tcc gtg ata gta ctt gac ttt gtg tct cac gtg Gly Leu Ile Asn Asn Ser Val Ile Val Leu Asp Phe Val Ser His Val 395 400 405			1312
aat tac acc ttt gaa ata gaa gca atg aat gga gtt tct gag ttg agt Asn Tyr Thr Phe Glu Ile Glu Ala Met Asn Gly Val Ser Glu Leu Ser 410 415 420 425			1360
ttt tct ccc aag cca ttc aca gct att aca gtg acc acg gat caa gat Phe Ser Pro Lys Pro Phe Thr Ala Ile Thr Val Thr Thr Asp Gln Asp 430 435 440			1408
gca cct tcc ctg ata ggt gtg gta agg aag gac tgg gca tcc caa aat Ala Pro Ser Leu Ile Gly Val Val Arg Lys Asp Trp Ala Ser Gln Asn 445 450 455			1456
agc att gcc cta tca tgg caa gca cct gct ttt tcc aat gga gcc att Ser Ile Ala Leu Ser Trp Gln Ala Pro Ala Phe Ser Asn Gly Ala Ile 460 465 470			1504
ctg gac tac gag atc aag tac tat gag aaa gaa cat gag cag ctg acc Leu Asp Tyr Glu Ile Lys Tyr Tyr Glu Lys Glu His Glu Gln Leu Thr 475 480 485			1552

tac tct tcc aca agg tcc aaa gcc ccc agt gtc atc atc aca ggt ctt Tyr Ser Ser Thr Arg Lys Tyr Val Phe His Ile Arg Val Arg Thr Ala Thr 490 495 500 505	1600
aag cca gcc acc aaa tat gta ttt cac atc cga gtg aga act gcg aca Lys Pro Ala Thr Lys Tyr Val Phe His Ile Arg Val Arg Thr Ala Thr 510 515 520	1648
gga tac agt ggc tac agt cag aaa ttt gaa ttt gaa aca gga gat gaa Gly Tyr Ser Gly Tyr Ser Gln Lys Phe Glu Phe Glu Thr Gly Asp Glu 525 530 535	1696
act tct gac atg gca gca gaa caa gga cag att ctc gtg ata gcc acc Thr Ser Asp Met Ala Ala Glu Gln Gly Gln Ile Leu Val Ile Ala Thr 540 545 550	1744
gcc gct gtt ggc gga ttc act ctc ctc gtc atc ctc act tta ttc ttc Ala Ala Val Gly Gly Phe Thr Leu Leu Val Ile Leu Thr Leu Phe Phe 555 560 565	1792
ttg atc act ggg aga tgt cag tgg tac ata aaa gcc aag atg aag tca Leu Ile Thr Gly Arg Cys Gln Trp Tyr Ile Lys Ala Lys Met Lys Ser 570 575 580 585	1840
gaa gag aag aga aga aac cac tta cag aat ggg cat ttg cgc ttc ccg Glu Glu Lys Arg Arg Asn His Leu Gln Asn Gly His Leu Arg Phe Pro 590 595 600	1888
gga att aaa act tac att gat cca gat aca tat gaa gac cca tcc cta Gly Ile Lys Thr Tyr Ile Asp Pro Asp Thr Tyr Glu Asp Pro Ser Leu 605 610 615	1936
gca gtc cat gaa ttt gca aag gag att gat ccc tca aga att cgt att Ala Val His Glu Phe Ala Lys Glu Ile Asp Pro Ser Arg Ile Arg Ile 620 625 630	1984
gag aga gtc att ggg gca ggt gaa ttt gga gaa gtc tgt agt ggg cgt Glu Arg Val Ile Gly Ala Gly Glu Phe Gly Glu Val Cys Ser Gly Arg 635 640 645	2032
ttg aag aca cca ggg aaa aga gag atc cca gtt gcc att aaa act ttg Leu Lys Thr Pro Gly Lys Arg Glu Ile Pro Val Ala Ile Lys Thr Leu 650 655 660 665	2080
aaa ggt ggc cac atg gat cgg caa aga aga gat ttt cta aga gaa gct Lys Gly Gly His Met Asp Arg Gln Arg Arg Asp Phe Leu Arg Glu Ala 670 675 680	2128
agt atc atg ggc cag ttt gac cat cca aac atc att cgc cta gaa ggg Ser Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile Arg Leu Glu Gly 685 690 695	2176
gtt gtc acc aaa aga tcc ttc ccg gcc att ggg gtg gag gcg ttt tgc Val Val Thr Lys Arg Ser Phe Pro Ala Ile Gly Val Glu Ala Phe Cys 700 705 710	2224
ccc agc ttc ctg agg gca ggg ttt tta aat agc atc cag gcc ccg cat Pro Ser Phe Leu Arg Ala Gly Phe Leu Asn Ser Ile Gln Ala Pro His 715 720 725	2272
cca gtg cca ggg gga gga tct ttg ccc ccc agg att cct gct ggc aga Pro Val Pro Gly Gly Ser Leu Pro Pro Arg Ile Pro Ala Gly Arg 730 735 740 745	2320
cca gta atg att gtg gtg gaa tat atg gag aat gga tcc cta gac tcc Pro Val Met Ile Val Val Glu Tyr Met Glu Asn Gly Ser Leu Asp Ser 750 755 760	2368
ttt ttg cgg aag cat gat ggc cac ttc aca gtc atc cag ttg gtc gga Phe Leu Arg Lys His Asp Gly His Phe Thr Val Ile Gln Leu Val Gly 765 770 775	2416
atg ctc cga ggc att gca tca ggc atg aag tat ctt tct gat atg ggt Met Leu Arg Gly Ile Ala Ser Gly Met Lys Tyr Leu Ser Asp Met Gly 780 785 790 795	2464

780	785	790	
tat gtt cat cga gac cta gcg gct cgg aat ata ctg gtc aat agc aac			2512
Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn			
795	800	805	
tta gta tgc aaa gtt tct gat ttt ggt ctc tcc aga gtg ctg gaa gat			2560
Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp			
810	815	820	825
gat cca gaa gct gct tat aca aca act ggt gga aaa atc ccc ata agg			2608
Asp Pro Glu Ala Pro Glu Tyr Thr Thr Thr Gly Gly Lys Ile Pro Ile Arg			
	830	835	840
tgg aca gcc cca gaa gcc atc gcc tac aga aaa ttc tcc tca gca agc			2656
Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Ser Ser Ala Ser			
	845	850	855
gat gca tgg agc tat ggc att gtc atg tgg gag gtc atg tcc tat gga			2704
Asp Ala Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr Gly			
	860	865	870
gag aga cct tat tgg gaa atg tct aac caa gat gtc att ctg tcc att			2752
Glu Arg Pro Tyr Trp Glu Met Ser Asn Gln Asp Val Ile Leu Ser Ile			
	875	880	885
gaa gaa ggg tac aga ctt cca gct ccc atg ggc tgt cca gca tct cta			2800
Glu Glu Gly Tyr Arg Leu Pro Ala Pro Met Gly Cys Pro Ala Ser Leu			
	890	895	900
cac cag ctg atg ctc cac tgc tgg cag aag gag aga aat cac aga cca			2848
His Gln Leu Met Leu His Cys Trp Gln Lys Glu Arg Asn His Arg Pro			
	910	915	920
aaa ttt act gac att gtc agc ttc ctt gac aaa ctg atc cga aat ccc			2896
Lys Phe Thr Asp Ile Val Ser Phe Leu Asp Lys Leu Ile Arg Asn Pro			
	925	930	935
agt gcc ctt cac acc ctg gtg gag gac atc ctt gta atg cca gag tcc			2944
Ser Ala Leu His Thr Leu Val Glu Asp Ile Leu Val Met Pro Glu Ser			
	940	945	950
cct ggt gaa gtt ccg gaa tat cct ttg ttt gtc aca gtt ggt gac tgg			2992
Pro Gly Glu Val Pro Glu Tyr Pro Leu Phe Val Thr Val Gly Asp Trp			
	955	960	965
cta gat tct ata aag atg ggg caa tac aag aat aac ttc gtg gca gca			3040
Leu Asp Ser Ile Lys Met Gly Gln Tyr Lys Asn Asn Phe Val Ala Ala			
	970	975	980
ggg ttt aca aca ttt gac ctg att tca aga atg agc att gat gac att			3088
Gly Phe Thr Thr Phe Asp Leu Ile Ser Arg Met Ser Ile Asp Asp Ile			
	990	995	1000
aga aga att gga gtc ata ctt att gga cac cag aga cga ata gtc			3133
Arg Arg Ile Gly Val Ile Leu Ile Gly His Gln Arg Arg Ile Val			
	1005	1010	1015
agc agc ata cag act tta cgt tta cac atg atg cac ata cag gag			3178
Ser Ser Ile Gln Thr Leu Arg Leu His Met Met His Ile Gln Glu			
	1020	1025	1030
aag gga ttt cat gta tga aagtaaccaca agcacctgtg ttttgtgcct			3226
Lys Gly Phe His Val			
	1035		
cagcatttct aaaatgaacg atatactctc tactactctc tcttctgatt ctccaaacat			3286
cacttcacaa actgcagtct tctgttcaga ctataggcac acaccttatg tttatgcttc			3346
caaccaggat tttaaaatca tgctacataa atccgttctg aataacctgc aactaaaacc			3406
ctggcccaact gcagattatt gctacgcaat ggtaaataac tcagcatgga tgtgtaattt			3466

16U 102 R1.ST25

```

tgtataagcc gtatatggga agtgttcacg gacttaacct aaaaaaattt atccaggtgg 3526
ggcttcctta gtgatgtatg tagagtgtga tggtagatga gaaagaacta gttgaccttt 3586
ctttcatgtt ttgtgatcaa gtagcttcca aactgacaga aatgtttcat ttttagataa 3646
ttatatcag ctctattggt tgtattatta ctttattttt taatacttta actgttggtg 3706
cctgatattg ttagaattat ttgcagaaat gaccagtgat atcatgtaat gaatttttgt 3766
gaggtatgac tatggtgaga aggggggttat tagggagggg gaaaaaata ctgtgtttat 3826
aaatctaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3886
aaaaaaaaaa aaaaaaaaaa aaaaaaaa 3914

```

<210> 2  
 <211> 1036  
 <212> PRT  
 <213> Homo sapien

<400> 2

Met Gly Gly Cys Glu Val Arg Glu Phe Leu Leu Gln Phe Gly Phe Phe  
 1 5 10 15

Leu Pro Leu Leu Thr Ala Trp Pro Gly Asp Cys Ser His Val Ser Asn  
 20 25 30

Asn Gln Val Val Leu Leu Asp Thr Thr Thr Val Leu Gly Glu Leu Gly  
 35 40 45

Trp Lys Thr Tyr Pro Leu Asn Gly Trp Asp Ala Ile Thr Glu Met Asp  
 50 55 60

Glu His Asn Arg Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Glu  
 65 70 75 80

Pro Asn Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala  
 85 90 95

Ala Gln Lys Ile Tyr Val Glu Met Lys Phe Thr Leu Arg Asp Cys Asn  
 100 105 110

Ser Ile Pro Trp Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Phe  
 115 120 125

Tyr Met Glu Ser Asp Glu Ser His Gly Ile Lys Phe Lys Pro Asn Gln  
 130 135 140

Tyr Thr Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met  
 145 150 155 160

Asp Leu Gly Asp Arg Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val  
 165 170 175

Gly Pro Ile Glu Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly  
 180 185 190

Ala Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro  
 195 200 205

Phe Thr Val Arg Asn Leu Ala Met Phe Pro Asp Thr Ile Pro Arg Val  
 210 215 220

Asp Ser Ser Ser Leu Val Glu Val Arg Gly Ser Cys Val Lys Ser Ala  
 225 230 235 240

Glu Glu Arg Asp Thr Pro Lys Leu Tyr Cys Gly Ala Asp Gly Asp Trp  
 245 250 255

Leu Val Pro Leu Gly Arg Cys Ile Cys Ser Thr Gly Tyr Glu Glu Ile  
 260 265 270

Glu Gly Ser Cys His Ala Cys Arg Pro Gly Phe Tyr Lys Ala Phe Ala  
 275 280 285

Gly Asn Thr Lys Cys Ser Lys Cys Pro Pro His Ser Leu Thr Tyr Met  
 290 295 300

Glu Ala Thr Ser Val Cys Gln Cys Glu Lys Gly Tyr Phe Arg Ala Glu  
 305 310 315 320

Lys Asp Pro Pro Ser Met Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg  
 325 330 335

Asn Val Val Phe Asn Ile Asn Glu Thr Ala Leu Ile Leu Glu Trp Ser  
 340 345 350

Pro Pro Ser Asp Thr Gly Gly Arg Lys Asp Leu Thr Tyr Ser Val Ile  
 355 360 365

Cys Lys Lys Cys Gly Leu Asp Thr Ser Gln Cys Glu Asp Cys Gly Gly  
 370 375 380

Gly Leu Arg Phe Ile Pro Arg His Thr Gly Leu Ile Asn Asn Ser Val  
 385 390 395 400

Ile Val Leu Asp Phe Val Ser His Val Asn Tyr Thr Phe Glu Ile Glu  
 405 410 415

Ala Met Asn Gly Val Ser Glu Leu Ser Phe Ser Pro Lys Pro Phe Thr  
 420 425 430

Ala Ile Thr Val Thr Thr Asp Gln Asp Ala Pro Ser Leu Ile Gly Val  
 435 440 445

Val Arg Lys Asp Trp Ala Ser Gln Asn Ser Ile Ala Leu Ser Trp Gln  
 450 455 460

Ala Pro Ala Phe Ser Asn Gly Ala Ile Leu Asp Tyr Glu Ile Lys Tyr  
 465 470 475 480

Tyr Glu Lys Glu His Glu Gln Leu Thr Tyr Ser Ser Thr Arg Ser Lys  
 485 490 495

Ala Pro Ser Val Ile Ile Thr Gly Leu Lys Pro Ala Thr Lys Tyr Val  
500 505 510

Phe His Ile Arg Val Arg Thr Ala Thr Gly Tyr Ser Gly Tyr Ser Gln  
515 520 525

Lys Phe Glu Phe Glu Thr Gly Asp Glu Thr Ser Asp Met Ala Ala Glu  
530 535 540

Gln Gly Gln Ile Leu Val Ile Ala Thr Ala Ala Val Gly Gly Phe Thr  
545 550 555 560

Leu Leu Val Ile Leu Thr Leu Phe Phe Leu Ile Thr Gly Arg Cys Gln  
565 570 575

Trp Tyr Ile Lys Ala Lys Met Lys Ser Glu Glu Lys Arg Arg Asn His  
580 585 590

Leu Gln Asn Gly His Leu Arg Phe Pro Gly Ile Lys Thr Tyr Ile Asp  
595 600 605

Pro Asp Thr Tyr Glu Asp Pro Ser Leu Ala Val His Glu Phe Ala Lys  
610 615 620

Glu Ile Asp Pro Ser Arg Ile Arg Ile Glu Arg Val Ile Gly Ala Gly  
625 630 635 640

Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Thr Pro Gly Lys Arg  
645 650 655

Glu Ile Pro Val Ala Ile Lys Thr Leu Lys Gly Gly His Met Asp Arg  
660 665 670

Gln Arg Arg Asp Phe Leu Arg Glu Ala Ser Ile Met Gly Gln Phe Asp  
675 680 685

His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Lys Arg Ser Phe  
690 695 700

Pro Ala Ile Gly Val Glu Ala Phe Cys Pro Ser Phe Leu Arg Ala Gly  
705 710 715 720

Phe Leu Asn Ser Ile Gln Ala Pro His Pro Val Pro Gly Gly Gly Ser  
725 730 735

Leu Pro Pro Arg Ile Pro Ala Gly Arg Pro Val Met Ile Val Val Glu  
740 745 750

Tyr Met Glu Asn Gly Ser Leu Asp Ser Phe Leu Arg Lys His Asp Gly  
755 760 765

His Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ser  
770 775 780

Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp Leu Ala  
785 790 795 800

Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp  
805 810 815

Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr  
820 825 830

Thr Thr Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile  
835 840 845

Ala Tyr Arg Lys Phe Ser Ser Ala Ser Asp Ala Trp Ser Tyr Gly Ile  
850 855 860

Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Glu Met  
865 870 875 880

Ser Asn Gln Asp Val Ile Leu Ser Ile Glu Glu Gly Tyr Arg Leu Pro  
885 890 895

Ala Pro Met Gly Cys Pro Ala Ser Leu His Gln Leu Met Leu His Cys  
900 905 910

Trp Gln Lys Glu Arg Asn His Arg Pro Lys Phe Thr Asp Ile Val Ser  
915 920 925

Phe Leu Asp Lys Leu Ile Arg Asn Pro Ser Ala Leu His Thr Leu Val  
930 935 940

Glu Asp Ile Leu Val Met Pro Glu Ser Pro Gly Glu Val Pro Glu Tyr  
945 950 955 960

Pro Leu Phe Val Thr Val Gly Asp Trp Leu Asp Ser Ile Lys Met Gly  
965 970 975

Gln Tyr Lys Asn Asn Phe Val Ala Ala Gly Phe Thr Thr Phe Asp Leu  
980 985 990

Ile Ser Arg Met Ser Ile Asp Asp Ile Arg Arg Ile Gly Val Ile Leu  
995 1000 1005

Ile Gly His Gln Arg Arg Ile Val Ser Ser Ile Gln Thr Leu Arg  
1010 1015 1020

Leu His Met Met His Ile Gln Glu Lys Gly Phe His Val  
1025 1030 1035

<210> 3  
<211> 1035  
<212> PRT  
<213> Mus musculus

<400> 3

Met Gly Gly Cys Glu Val Arg Glu Phe Leu Leu Gln Phe Gly Phe Phe  
1 5 10 15

Leu Pro Leu Leu Thr Ala Trp Thr Gly Asp Cys Ser His Val Ser Asn  
20 25 30



Gln Val Val Leu Leu Asp Thr Thr Thr Val Met Gly Glu Leu Gly Trp  
 35 40 45  
 Lys Thr Tyr Pro Leu Asn Gly Trp Asp Ala Ile Thr Glu Met Asp Glu  
 50 55 60  
 His Asn Arg Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Glu Pro  
 65 70 75 80  
 Asn Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala Ala  
 85 90 95  
 Gln Lys Ile Tyr Val Glu Met Lys Phe Thr Leu Arg Asp Cys Asn Ser  
 100 105 110  
 Ile Pro Trp Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr  
 115 120 125  
 Ile Glu Ser Asp Glu Ser His Gly Thr Lys Phe Lys Pro Ser Gln Tyr  
 130 135 140  
 Ile Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp  
 145 150 155 160  
 Leu Gly Asp Arg Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly  
 165 170 175  
 Pro Ile Glu Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala  
 180 185 190  
 Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Phe  
 195 200 205  
 Thr Val Arg Ser Leu Ala Met Phe Pro Asp Thr Ile Pro Arg Val Asp  
 210 215 220  
 Ser Ser Ser Leu Val Glu Val Arg Gly Ser Cys Val Lys Ser Ala Glu  
 225 230 235 240  
 Glu Arg Asp Thr Pro Lys Leu Tyr Cys Gly Ala Asp Gly Asp Trp Leu  
 245 250 255  
 Val Pro Leu Gly Arg Cys Ile Cys Ser Thr Gly Tyr Glu Glu Ile Glu  
 260 265 270  
 Gly Ser Cys His Ala Cys Arg Pro Gly Phe Tyr Lys Ala Phe Ala Gly  
 275 280 285  
 Asn Thr Lys Cys Ser Lys Cys Pro Pro His Ser Ser Thr Tyr Val Glu  
 290 295 300  
 Ala Thr Ser Val Cys His Cys Glu Lys Gly Tyr Phe Arg Ala Glu Lys  
 305 310 315 320  
 Asp Pro Pro Ser Met Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg Asn  
 325 330 335  
 Val Ala Phe Asn Ile Asn Glu Thr Ala Leu Ile Leu Glu Trp Ser Pro  
 340 345 350  
 Pro Ser Asp Thr Gly Gly Arg Lys Asp Leu Thr Tyr Ser Val Ile Cys  
 355 360 365  
 Lys Lys Cys Gly Leu Asp Thr Thr Gln Cys Glu Asp Cys Gly Gly Gly  
 370 375 380  
 Leu Arg Phe Ile Pro Arg His Thr Gly Leu Ile Asn Asn Ser Val Val  
 385 390 395 400  
 Val Leu Asp Phe Val Ser His Val Asn Tyr Thr Phe Glu Ile Glu Ala  
 405 410 415  
 Met Asn Gly Val Ser Glu Leu Ser Ile Ser Pro Lys Pro Phe Thr Ala

420

425

430

Ile Thr Val Thr Thr Asp His Asp Ala Pro Ser Leu Ile Gly Met Met  
 435 440 445  
 Arg Lys Asp Trp Ala Ser Gln Asn Ser Leu Ala Leu Ser Trp Gln Ala  
 450 455 460  
 Pro Ala Phe Ser Asn Gly Ala Ile Leu Asp Tyr Glu Thr Lys Tyr Tyr  
 465 470 475 480  
 Glu Lys Glu His Glu Gln Leu Thr Tyr Ser Ser Thr Arg Ser Lys Ala  
 485 490 495  
 Pro Ser Val Ile Val Thr Gly Leu Lys Pro Ala Thr Thr Tyr Ile Phe  
 500 505 510  
 His Ile Arg Val Arg Thr Ala Thr Gly Tyr Ser Gly Tyr Ser Gln Lys  
 515 520 525  
 Phe Glu Phe Glu Thr Gly Asp Glu Thr Ser Asp Met Ala Ala Glu Gln  
 530 535 540  
 Gly Gln Ile Leu Val Ile Ala Thr Ala Ala Val Gly Gly Phe Thr Leu  
 545 550 555 560  
 Leu Val Ile Leu Thr Leu Phe Phe Leu Ile Thr Gly Arg Cys Gln Trp  
 565 570 575  
 Tyr Ile Lys Ala Lys Met Lys Ser Glu Glu Lys Arg Arg Thr His Leu  
 580 585 590  
 Gln Asn Gly His Leu Arg Phe Pro Gly Ile Lys Thr Tyr Ile Asp Pro  
 595 600 605  
 Asp Thr Tyr Glu Asp Pro Ser Leu Ala Val His Glu Phe Ala Lys Glu  
 610 615 620  
 Ile Asp Pro Ser Arg Ile Arg Ile Glu Arg Val Ile Gly Ala Gly Glu  
 625 630 635 640  
 Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Thr Pro Gly Lys Arg Glu  
 645 650 655  
 Ile Pro Val Ala Ile Lys Thr Leu Lys Gly Gly His Met Asp Arg Gln  
 660 665 670  
 Arg Arg Asp Phe Leu Arg Glu Ala Ser Ile Met Gly Gln Phe Asp His  
 675 680 685  
 Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Lys Arg Ser Phe Pro  
 690 695 700  
 Ala Ile Gly Val Glu Ala Phe Cys Pro Ser Phe Leu Arg Ala Gly Phe  
 705 710 715 720  
 Leu Asn Gly Ile Gln Ala Pro His Pro Val Thr Ala Gly Gly Ser Leu  
 725 730 735  
 Pro Pro Arg Ile Pro Ala Gly Arg Pro Val Met Ile Val Val Glu Tyr  
 740 745 750  
 Met Glu Asn Gly Ser Leu Asp Ser Phe Leu Arg Lys His Asp Gly His  
 755 760 765  
 Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ser Gly  
 770 775 780  
 Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp Leu Ala Ala  
 785 790 795 800  
 Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe  
 805 810 815

16U 102 R1.ST25

Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr  
820 825 830

Thr Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala  
835 840 845

Tyr Arg Lys Phe Ser Ser Ala Ser Asp Ala Trp Ser Tyr Gly Ile Val  
850 855 860

Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Glu Met Ser  
865 870 875 880

Asn Gln Asp Val Ile Leu Ser Ile Glu Glu Gly Tyr Arg Leu Pro Ala  
885 890 895

Pro Met Gly Cys Pro Pro Ser Leu Gln Gln Leu Met Leu His Cys Trp  
900 905 910

Gln Lys Glu Arg Asn His Arg Pro Lys Phe Thr Asp Ile Val Ser Phe  
915 920 925

Leu Asp Lys Leu Ile Arg Asn Pro Ser Ala Leu His Thr Leu Val Glu  
930 935 940

Asp Ile Leu Val Met Pro Glu Ser Pro Gly Asp Val Pro Glu Tyr Pro  
945 950 955 960

Leu Phe Val Thr Val Gly Asp Trp Leu Asp Ser Ile Lys Met Gly Gln  
965 970 975

Tyr Lys Ser Asn Phe Met Ala Ala Gly Phe Thr Thr Phe Asp Leu Ile  
980 985 990

Ser Arg Met Ser Ile Asp Asp Ile Arg Arg Ile Gly Val Ile Leu Ile  
995 1000 1005

Gly His Gln Arg Arg Ile Val Ser Ser Ile Gln Thr Leu Arg Leu  
1010 1015 1020

His Met Met His Ile Gln Glu Lys Gly Phe His Val  
1025 1030 1035

<210> 4

<211> 3604

<212> DNA

<213> Mus musculus

<400> 4

aggaccccca cgctactagg aacacctggc tgcgctgctg ccacttcttt ttaaggagga 60  
gaagagaacc aaccagagcc atggggggct gcgaagtccg ggaatttctt ttgcaatttg 120  
gtttcttctt gccctgcta acggcttga cggcgactg cagtcacgtc tccaaccaag 180  
ttgtgttgc tgaacaacc acagtgatg gagaactagg atggaaaaca tatccattaa 240  
atgggtggga tgccattact gaaatggatg aacacaatag gccatacat acataccagg 300  
tatgcaatgt catggaacca aaccagaaca actggcttcg tactaactgg atctctcgtg 360  
atgctgcaca gaaaatttat gtggaatga agttcacact gagggattgt aacagcatcc 420  
catgggtctt ggggacttgt aaagaaacct ttaacctgta ttatatagaa tccgatgaat 480  
cccatgggac aaaattcaag ccaagccaat atataaagat cgacacaatt. gctgctgatg 540  
agagttttac tcagatggat ttgggtgacc gcataccttaa actcaacact gaaatccgtg 600  
agggtgggcc tatagaaagg aaaggatttt atttggtttt tcaagatatt ggagcatgca 660  
tcgctctggt ctacgtccga gttttctaca aaaaatgccc cttcacctg cgagacttgg 720  
ctatgtttcc tgataccatc ccaagggttg attcttctc tttggttgaa gtgcggggct 780

catgtgtaaa gagtgctgag gagcgagata ctcttaaact ctactgtgga gctgatggg	840
attggcttgt tcctcttga aggtgtatct gcagtacagg gtatgaagaa atcgagggtt	900
cttgccatgc ttgcagacca ggattctaca aagcatttgc tgggaacaca aaagttccaa	960
atgccctcca cacagctcaa cctacgtgga agcaacgtca gtctgtcatt gtgaaaagg	1020
ttacttccgg gcagaaaaag acccaccttc tatggcatgc actagaccac cttcagctcc	1080
tagaaatgtg gcttttaaca tcaatgaaac agcccttatt ttggaatgga gccacccag	1140
tgacacagga gggagaaaag atctcacata cagtgtaatc tgtaagaaat gtggtttaga	1200
cactaccag tgtgaggact gtggtggagg actccgcttc atcccaagac aactggact	1260
gatcaacaat tctgtggtag tactggactt tgtgtctcac gtcaattata cttttgaaat	1320
agaagccatg aatggagttt ctgagttgag catctctccc aagccattca cagctattac	1380
agtgactaca gatcacgatg caccttctct gattggtatg atgagaaagg actgggcatc	1440
tcagaacagc cttgctctat cgtggcaagc acctgcattt tccaatggag ctattctgga	1500
ctatgagacc aagtactacg agaaagagca tgagcagctc acctattcct ccacgaggtc	1560
caaggcccca agcgtcatcg tcacgggcct caagcccgc accacgtaca tatttcacat	1620
ccgagtgagg acggcgacag gctacagtgg ctacagtcag aagtttgaat ttgaaacagg	1680
agatgaaact tctgacatgg cggcagaaca agggcagatt ctggtcatag ccactgcagc	1740
cgctcgggga ttactctct tagtcctct caccctgttc ttctcatca ctgggaggtg	1800
tcaatggtac ataaaggcca aaatgaagtc agaagagaag agaagaactc acttacagaa	1860
cgccacctg cgcttcccg gaattaaaac atacattgat ccagacacct atgaagacc	1920
tatccctagca gtccacgaat ttgcaaaaga gattgatcct tcaagaattc gcattgagag	1980
agtgattgga gcaggtgaat ttggagaagt ctgcagtggg cgtttgaaga caccagggaa	2040
aaaggagatc ccagttgcaa ttaaaacatt gaaagggtgc cacatggacc gacaaagaag	2100
agattttcta agagaagcta gcatcatggg tcagtttgac cacccaaaca tcattcgctt	2160
agaaggtgtt gtcactaaaa gatccttccc ggcgattggg gtggaagcct tctgccccag	2220
cttcttaagg gctgggtttt taaatggcat ccaagcacca catccagtga ctgcaggagg	2280
ctctctgccc ccaggatct ctgcaggtcg gccagtaatg atcgtagtag agtatatgga	2340
gaatggatca ctggactcct ttttgcgaa gcatgatggc cacttcaccg tcatccagtt	2400
ggtcggcatg ctgaggggca tcgcgtcagg catgaagtat ctttctgaca tgggatatgt	2460
tcatcgagat cttgccgca ggaacatact ggtgaacagc aacttagtat gcaaggcttc	2520
tgatttttgt ctctcccgag tgctggaaga tgatccagaa gcagcttata caacaacggg	2580
agggaaaatc cctatacggg ggacagcccc agaagctatt gcttacagaa agttctcttc	2640
agccagtgc gcgtggagct acgggattgt catgtgggag gtgatgtcct atggagagag	2700
accgtactgg gaaatgtcca accaggatgt tatcttgtcc attgaagaag gttaccgact	2760
tcctgtctcg atgggtgcc caccatctct gcaacagctg atgtccact gctggcagaa	2820
ggagagaaac cacaggccaa aattcactga catcgtcagc ttcttgaca aactgatccg	2880
caacccagtc gcccttcaca cgctggtgga ggacatcctt gtaatgccag aatcccctgg	2940
tgatgttctt gaatatccat tgtttgtcac agtaggtgac tggctggatt ctataaagat	3000

16U 102 R1.ST25

```

ggggcaatac aagagtaact tcatggcagc gggttttaca acgtttgatc tgatttcacg 3060
aatgagcatc gatgatatta ggcgaattgg agtcattctc attggacatc agagacgaat 3120
agtcagcagc atacaaactt tacgtttaca tatgatgcac atacaggaaa aaggatttca 3180
tgtatgaaag tactataaac acctgtatct tgtgcctcag cattttctaca aagaaagata 3240
ttccctctac gactcattct tctgattctc cagccttccc ttcaccaccc accgtctcct 3300
gttccgacta tggctgcaca ccttacgttt atgcttcac cctggatttc aataccacgc 3360
tacacaggtc ctctctgaat agcctgcaa cgaactctg gccactgca gatcatcact 3420
gcagaacgat aaataactca gcatgaatgt gtaactttgt acagaaatgt ttgggaagtg 3480
ttcatggact tcacctaaag gaatttgtcc ttaagtgtgg catcttcaga gacgtgtgtg 3540
gagtttgatg atagataaga agaaaatagc tgatcattct tccatgtttt gtgatcgagt 3600
agct 3604

```

```

<210> 5
<211> 334
<212> PRT
<213> Homo sapiens
<220>
<221> MISC_FEATURE
<222> (3)..(24)
<223> X=unsure

```

> 5

```

Met Lys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1      5      10      15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ser Asp Met Ala Ala Glu Gln Gly
20      25      30
Gln Ile Leu Val Ile Ala Thr Ala Ala Val Gly Gly Phe Thr Leu Leu
35      40      45
Val Ile Leu Thr Leu Phe Phe Leu Ile Thr Gly Arg Cys Gln Trp Tyr
50      55      60
Ile Lys Ala Lys Met Lys Ser Glu Glu Lys Arg Arg Asn His Leu Gln
65      70      75      80
Asn Gly His Leu Arg Phe Pro Gly Ile Lys Thr Tyr Ile Asp Pro Asp
85      90      95
Thr Tyr Glu Asp Pro Ser Leu Ala Val His Glu Phe Ala Lys Glu Ile
100     105     110
Asp Pro Ser Arg Ile Arg Ile Glu Arg Val Ile Gly Ala Gly Glu Phe
115     120     125
Gly Glu Val Cys Ser Gly Arg Leu Lys Thr Pro Gly Lys Arg Glu Ile
130     135     140
Pro Val Ala Ile Lys Thr Leu Lys Gly Gly His Met Asp Arg Gln Arg
145     150     155     160
Arg Asp Phe Leu Arg Glu Ala Ser Ile Met Gly Gln Phe Asp His Pro
165     170     175
Asn Ile Ile Arg Leu Glu Gly Val Val Thr Lys Arg Ser Phe Pro Ala
180     185     190
Ile Gly Val Glu Ala Phe Cys Pro Ser Phe Leu Arg Ala Gly Phe Leu
195     200     205

```

Asn Ser Ile Gln Ala Pro His Pro Val Pro Gly Gly Gly Ser Leu Pro  
 210 215 220  
 Pro Arg Ile Pro Ala Gly Arg Pro Val Met Ile Val Val Glu Tyr Met  
 225 230 235 240  
 Glu Asn Gly Ser Leu Asp Ser Phe Leu Arg Lys His Asp Gly His Phe  
 245 250 255  
 Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ser Gly Met  
 260 265 270  
 Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp Leu Ala Ala Arg  
 275 280 285  
 Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly  
 290 295 300  
 Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Thr  
 305 310 315 320  
 Asp Leu Phe Gln Thr Leu Thr Leu Asn Leu Cys Tyr Ser Ala  
 325 330

<210> 6  
 <211> 1583  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (339)..(402)  
 <223> n=unsure

<400> 6  
 agacaacaa aactacaatg gaagaagaaa acgtcctcaa ctagacatct gccaaaaata 60  
 tcattccagaa tgccttgga agttcacttc catttagtga agtgagataa tttggcaatt 120  
 cacgcaagag actgagaacc aagcctcaag ccctgcctct gattctgcag gtatggaaca 180  
 tgagcagctg acctactctt ccacaaggtc caaagcccc agtgtcatca tcacaggtct 240  
 taagccagcc accaaatatg tatttcacat ccgagtgaga actgcgacag gatacagtg 300  
 ctacagtcag aaatttgaat ttgaaacagg agatgaaann nnnnnnnnnn nnnnnnnnnn 360  
 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nncttctgac atggcagcag 420  
 aacaaggaca gattctcgtg atagccaccg ccgctgttgg cggattcact ctctcgtca 480  
 tcctcacttt attcttcttg atcactggga gatgtcagtg gtacataaaa gccaatga 540  
 agtcagaaga gaagagaaga aaccacttac agaatgggca tttgcgcttc ccggaatta 600  
 aaacttacat tgatccagat acatatgaag acccatccct agcagtcctt gaatttgcaa 660  
 aggagattga tccctcaaga attcgtattg agagagtcatt tggggcaggt gaatttgag 720  
 aagtctgtag tgggcgtttg aagacaccag ggaaaagaga gatcccagtt gccattaaaa 780  
 ctttgaaagg tggccacatg gatcggaaga gaagagattt tctaagagaa gctagtatca 840  
 tgggccagtt tgaccatcca aacatcatc gcctagaagg ggttgtcacc aaaagatcct 900  
 tcccgcccat tggggtggag gcgttttgcc ccagcttctt gagggcaggg tttttaaata 960  
 gcatccagc cccgcaccca gtgccagggg gaggatcttt gccccccagg attcctgctg 1020  
 gcagaccagt aatgattgtg gtggaatata tggagaatgg atccctagac tcctttttgc 1080  
 ggaagcatga tggccacttc acagtcattc agttggtcgg aatgctccga ggcattgcat 1140

16U 102 R1.ST25

caggcatgaa gtatctttct gatatgggtt atgttcacg agacctagcg gctcgggaata 1200  
 tactgggtcaa tagcaactta gtatgcaaag tttctgattt tggctctctcc agagtgtctgg 1260  
 aagatgatcc agaagctgct tataacaaca ctgacctctt ccaaactcta aacttaacc 1320  
 tctgctatct tgcataaatt ctgagaaaag ccaaattttc tgtcgggtcta agaagacata 1380  
 gcctacaccc aactggagat aattataaaa aataatgaag cagcatgagg ggaagggtatt 1440  
 taatgtgtat tttaaagttg ggagagattc tccttcacct aatttaggtg tttgtgaatt 1500  
 ggcttgactt ttggaagtta atttttaagc cttgaacatg tccaacttta agaactttaa 1560  
 gaataaatat tttaacacaa gtg 1583

<210> 7  
 <211> 24  
 <212> DNA  
 <213> Homo sapien

<400> 7  
 acaagggtcca aagccccag tgtc 24

<210> 8  
 <211> 25  
 <212> DNA  
 <213> Homo sapien

<400> 8  
 gcgcaaattgc ccattctgta agtgg 25

<210> 9  
 <211> 11  
 <212> PRT  
 <213> Homo sapien

<400> 9  
 Arg Glu Asn Ala Glu Tyr Leu Arg Val Ala Pro  
 1 5 10